

GAP of: 0964DU63530aa check: 7513 from: 1 to: 392

WPDEF Case 0964D Rad23 protein encoded by GenBank U63530 Rice Rad23

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SwissProt entry

Q40742

U63530. Oryza sativa osRA. . .[gi:1488296] Links

LOCUS OSU63530 1533 bp mRNA linear PLN 07-AUG-1997

DEFINITION Oryza sativa osRAD23 mRNA, complete cds. . . .

to: 0964sid4 check: 9188 from: 1 to: 368

WPDEF Case 0964 Rad23 SEQ ID NO: 4 corn

Case 0964 Rad23 SEQ ID NO: 4 corn

Symbol comparison table: blosum62.cmp CompCheck: 1102

BLOSUM62 amino acid substitution matrix.

Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid substitution matrices from protein blocks. Proc. Natl. Acad.

Sci. USA 89: 10915-10919.

Gap Weight: 8 Average Match: 2.778  
Length Weight: 2 Average Mismatch: -2.248

Quality: 861 Length: 394  
Ratio: 2.340 Gaps: 12  
Percent Similarity: 61.749 Percent Identity: 54.918

Match display thresholds for the alignment(s):

| = IDENTITY  
: = 2  
. = 1

0964DU63530aa x 0964sid4 October 28, 2003 11:26 ..

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1 MKISVKTLKGSTFQIEVDSAQKVADVVKRIETTQGGHIYPAEQQMLIHQG 50
  ||:|||||. |:| | : ||: || ||. || ||:| |
1 MKLTVKTLKGTHFEIRVQPNDTIMAVKKNIEEIQKDSYPWGQQLLIFNG 50

51 KVLKDDTTLDENKVLNSFLVIMLRQKGSSSSAPATSKAPSNQAPPTQT 100
  |||||:||||| |. |||:| |. | |. | |.
51 KVLKDESTLEENKVNEDGFLVVMLSKGKTSGST..GTSSSQHSNTPATRQ 98

101 VPAAPA.SQAPVAPATTVPVTVSAPTPTATASPAPAVAVSSEADNYGQAT 149
  | | ||| | |:| | | || | .. || |
99 APPLEAPQQAQPP..VAPITTSQP.....EGLPAQAPNTH.DN...AA 136

150 SNLVAGSNLEATIQSILEMGGGIWDRDIVLHALSAAFNNPERAVEYLYSG 199
  |||..| |:| | :||| | |:| | || |:| | | | | | | |
137 SNLLSGRNVDTIINQLMEMGGGSWDKDKVQRALRAAYNNPERAVEYLYSG 186

200 VPEQMDIPVPPPSIQPANPTQASQATQPAAPSILSSGPNASPLDLFPQAL 249
  :| :| | | | | | | | | | | | | | | | | | | | |
187 IPVTAEIAVPIGG.QGANTTDRA....PTGEAGLSGIPNTAPLDLFPQGA 231
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250 PNASTDAAAGLGNLDALRNNAQFRTLLSLVQANPQILQPLLQELGKQNPQI 299
    ||  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
232 SNAGGGAGG.GPLDFLRNNPQFQAVREMVHTNPQILQPMLVELSKQNPQI 280

300 LQLIQENQAEFLHLINEPAEGDDEENLLDQFPE.AMPQTIAVTPEEDEAI 348
    |.||:| | | | |:| | | | | | | | | | | | | | | | | | | | | |
281 LRLIEENHDEFLQLLNEPFEG.GEGDFLDQPEEDEMPHAISVTPEEQEAI 329

349 LRLEPMGFDRALVLDVFFACNKDEQLAANYLLDHMNEFADEGPP 392
    | | | | | | | | | |: | | | | | | | | | | | | | | | | | |
330 GRLESMGFDRARVIEAFLACDRNEELAANYLLEHAGE.ED.... 368

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